

Figure 1

hDEC2a

DEC1

MDEGIPHLQERQ—L——LEHRDFIGLDYSSLYMC-KPKRSMKRD-DTKDITYKLPHRLIEKKRRDRIN 61
M-ERIPSAQPPPAQLPKAPGLEHGDLPMPAHMYQVYKSRRGIKRSSEDSKETYLPHRLIEKKRRDRIN 69

ECIAQLKDLLPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIALQNG——ERSLKSPIQSD 127
ECIAQLKDLLPEHLKLTTLGHLEKAVVLELTCLKHVKALTNLIDQQQKIALQSGLQAGELSGR-NVETG 138

LDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGA——PS 194
QEMFCSGFQTCAREVLQYLAKHEN-T-RDLKSSQLVTHLHRVVSELLQGGTSRKPSDPAKVMDFKEKPS 206

A-A-GSAAAPCLERAGQKLEPLAYCVPVIQRTQP-SAELAAENDTDTDSGYGGAEARPD-R-E——K- 254
SPAKGSEG-P——G-K-N——CVPVIQRTFAHSSGEQSGSDTDTDSGYGGESEKG-DLRSEQPCFKS 263

—GK—GAGASRVTIKQEPPGEDSPAPK-RMKL-DSRGGG-SGGGPGGGAAAAAALLGPDPAALALLR 317
DHGRRFTMGERIGAIIKQESE-E-PPTKKNRMQLSDDEGHFTSS———D——— 305

PDAALLSSLVAFGGGGGAPFP-QPAAAAAPFCLPFCFLSP-SAAAAVQPFLLDKSGLEKYLPAAAAAAPF 385
——LISS—PFLG——PHHPQ——PFCLPF-YLIPPSATA-YL-PML——EKWYPTSV—P- 349

PLLYPGIPAPAAAAAAAAAAAAAAAAAFCLSSVLSPPPEKAGAAAATLL-PHEVAPLGAPHPQHHPGRTH 454
VL-YPGLNASAAA———LSSFMPN-DKISA—PLLMPQR——L—PSP——— 385

LPFAGPREPGNPSSA—QE-DPSQPGK-EA-P 482
LP-AHP——SVDSSVLLQALKPIPLNLETKD

(Homology 43%)

Figure 2

hDEC2a

hDEC2b

MDEGIPHLQERQLEHRDFIGLDYSSLYMCKPKRSMKRDDTK--DTYKLPRLIEKKRRDRINECIAQLK 68

MDEGIPHLQERQLEHRDFIGLDYSSLYMCKPKRSMKRDDTKVSOTYKLPRLIEKKRRDRINECIAQLK 70

DLLEPHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 138

DLLEPHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 140

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 208

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 210

QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGAEARPDKREKKGAGASRVTIKQEPPEGEDSPAPK 278

QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGAEARPDKREKKGAGASRVTIKQEPPEGEDSPAPK 280

RMKLDSRGGSGGGPGGGAAAAAALLGPDAAAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 348

RMKLDSRGGSGGGPGGGAAAAAALLGPDAAAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 350

LPFCFLSPSAAAAAYVQPFLLDKSGLEKYLPAAPAAAPFLLYPGIPAPAAAAAFAFCLSSV 418

LPFCFLSPSAAAAAYVQPFLLDKSGLEKYLPAAPAAAPFLLYPGIPAPAAAAAFAFCLSSV 420

LSPPPEKAGAAAATLLPHEVAPLGAPHPQHGRTHLPFAGPREPGNPESQAQEDPSQPGKEAP 482

LSPPPEKAGAAAATLLPHEVAPLGAPHPQHGRTHLPFAGPREPGNPESQAQEDPSQPGKEAP 484

Figure 3

hDEC2a

mDEC2a

MDEGIPHLQERQLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAWVLELT LKHLKALTALTEQQHQKIIALONGERSLKSPIQSDLDAFHSGFQTC AK 140

LPEHLKLTTLGHLEKAWVLELT LKHLKALTALTEQQHQKIIALONGERSLKSPVQADLDAFHSGFQTC AK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARP DREKKGAGASRVTIKQEPPEGDS-P 275

SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A--V--KQEP PG-DSSP 249

APKRMKLD SRGGSGGGPGGAAAAAALLGPDPA AAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAA 345

APKRPKLEARG-----ALLGPEPA-LL-G-SLVAL-GGGAPFAQPAAA- 288

PFCLPFCFLSPSAAAAYVQPF LDKSGLEKYL PAAAAAPFLLYPGIPAPAAAAA AF PCL 415

PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYL PAAAA-PFLLYPGIPA-----AAAAA AF PCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQH PHGRTHLPFAGPREPGNP ESSAQEDPSQPGKEAP 482

SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQH AHSRTHLPRAV-----NP ESS-QEDATQPAKDAP 410

Figure 4

hDEC2a
mDEC2a
SHARP-1

MDEGIPHLQERQQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70
MDEGIPHLQERQQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70
MDEGIPHLQERQQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTCAK 140
LPEHLKLTTLGHLEKAVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQADLDAFHSGFQTCAK 140
LPEHLKLTTLGHLEKAVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQADLDAFHSGFQTCAK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207
EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196
EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VT-PGRGPGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKKGAGASRVTIKQEPPGEDS-P 275
SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DSSP 249
SGS-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DPSL 249

APKRMKLSRGGGSGGGPGGGGAAAAAALLGPDAAAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAA 345
APKRPKLEARG-----ALLGPEPA-LL-G-SLVAL-GGGAPFAQPAAA- 288
RPRG 253

PFCLPFCFLSPSAAAAAYVQPFLOKSGLEKYLPAAPAAAPFLLYPGIPAPAAAAAFAFCL 415
PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLPAAPAAAPFLLYPGIPA-----AAAAAFAFCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPESQAQEDPSQPGKEAP 482
SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAV-----NPES-QEDATQPAKDAP 410